Ferret: a user-friendly tool to extract data from the 1000 Genomes Project

A. Taverner, O. Belkacem, E. Lam, N. Vince, P.-A. Gourraud, C. Winkler, M. Servières, Sophie Limou

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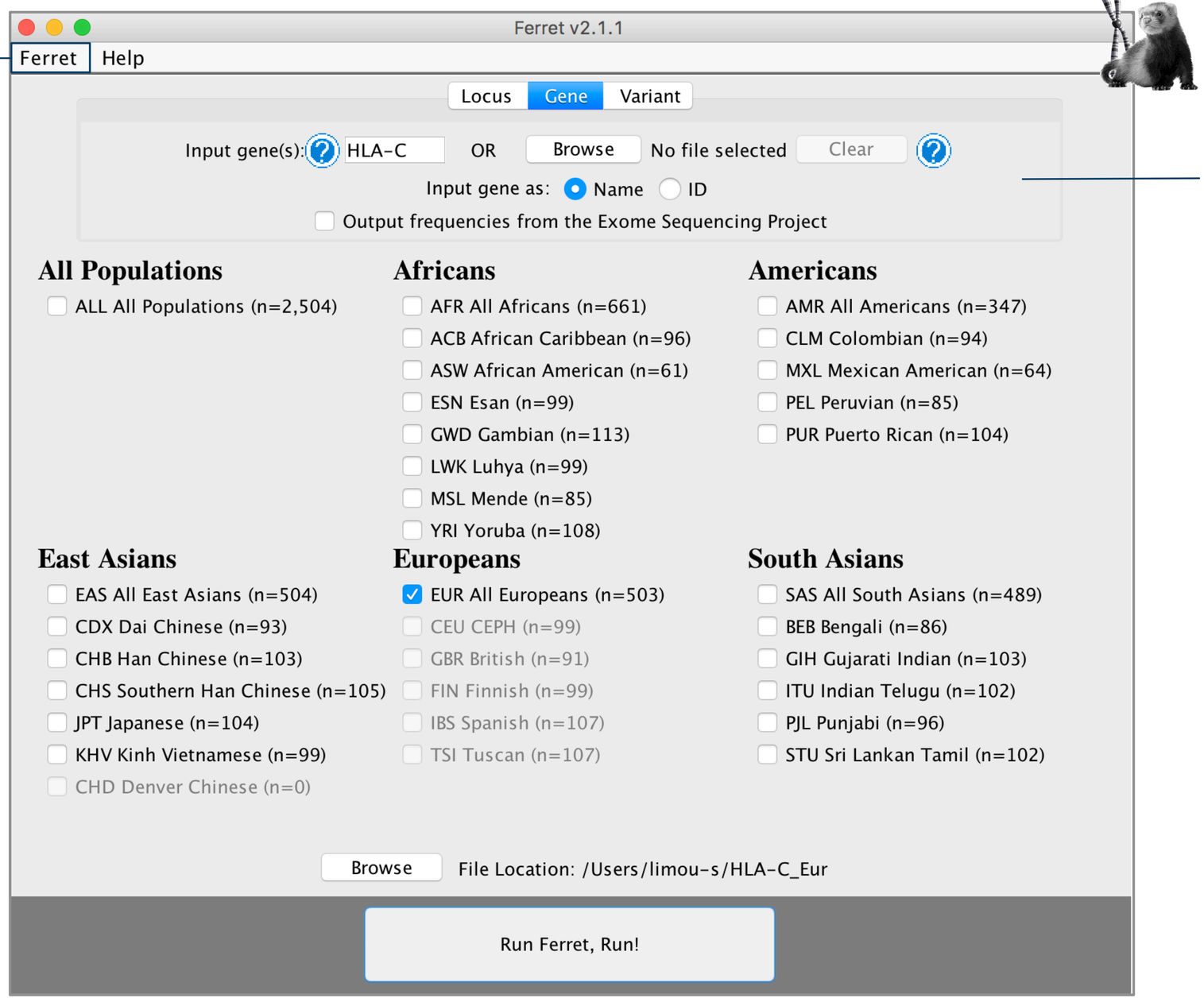
Contact:
sophie.limou@univ-nantes.fr
ferret@nih.gov

A. Taverner[1,2], O. Belkacem[3], E. Lam[3], N. Vince[4,5], PA. Gourraud[4,5], CA. Winkler[1], M. Servières[3], S. Limou[1,3-5]

[1]Basic Research Laboratory, NCI/NIH, Leidos Biomedical Research Inc., Frederick MD, USA
[2]Quantitative and Computational Biology program, Princeton University, Princeton NJ, USA
[3]Ecole Centrale de Nantes, Nantes, France
[4]Centre de Recherche en Transplantation et Immunologie (CRTI) UMR 1064, INSERM, Nantes, France
[5]Institut de Transplantation Urologie Néphrologie (ITUN), CHU Nantes, Nantes, France

Additional settings:
- Genome version
- Output format
- Frequency filter



Input flexibility:
- Locus position
- Gene
- Variant ID

Retrieve 1000 Genomes Project data
(and optionally Exome Sequencing Project –ESP– data)

.map file + .ped file → **PLINK files**: can be merged with user's dataset, etc.

.info file → **HaploView files**: data visualization, LD pattern, haplotypes, tagSNP design, etc.

.frq file → **Allele frequency file**

CHR	VARIANT	POS	A1	A2	NB_1KG_CHR	1KG_A1_FREQ	ESP6500_EA_A1_FREQ	ESP6500_AA_A1_FREQ
6	rs1065711	31236853	G	A	1006	0.1213	.	.
6	rs1049853	31236900	G	A	1006	0.8867	0.8726	0.9209
6	indel_rs41548117_TC/T	31237100	TC	T	1006	0.9553	0.9594	0.9183
6	rs41542414	31237766	A	T	1006	1	0.9995	0.9897
6	rs9264623	31237950	T	C	1006	0.2773	.	.
6	indel_rs9281300_C/CA	31239170	C	CA	1006	0.4195	0.535	0.4125

Unique advantages of Ferret[#]

- User-friendly interface
- Accepts input query as locus, gene(s), or variant(s)
- Handles SNPs and indels
- Outputs suitable for well-known pre-existing tools
- Computes allelic frequency for SNPs, indels and CNVs
- Retrieves allelic frequency from ESP
- **Dec. 2017 update**: sync with HaploView + gene borders

Perspectives (June 2018):
- Accelerate runtime speed
- Grant access to HLA alleles[§]
- Functional annotations

Publicly available at http://limousophie35.github.io/Ferret/

[#]Limou *et al.* Bioinformatics 2016;[§]Gourraud *et al.* PLoS One 2014